

**Raw Sequence Listing before editing  
(for reference only)**



IFWP

## RAW SEQUENCE LISTING

DATE: 10/06/2006

PATENT APPLICATION: US/10/594,118

TIME: 11:11:41

Input Set : A:\004974.01218 sequence listing.txt

Output Set: N:\CRF4\10062006\J594118.raw

2 <110> APPLICANT: Golz, Stefan  
 3 Bruggemeier, Ulf  
 4 Geerts, Andraese  
 6 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with  
 7 Peroxisome Proliferator Activated Receptor Delta (PPARD)  
 W--> 8 <130> FILE REFERENCE: 004974.01218  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/594,118  
 C--> 10 <141> CURRENT FILING DATE: 2006-09-25  
 10 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/002529  
 11 <151> PRIOR FILING DATE: 2005-03-10  
 13 <150> PRIOR APPLICATION NUMBER: EP 04007020.3  
 14 <151> PRIOR FILING DATE: 2004-03-24  
 16 <160> NUMBER OF SEQ ID NOS: 5  
 17 <170> SOFTWARE: PatentIn version 3.2

## ERRORED SEQUENCES

160 <210> SEQ ID NO: 5  
 161 <211> LENGTH: 24  
 162 <212> TYPE: DNA  
 163 <213> ORGANISM: artificial sequence  
 W--> 164 <220> FEATURE:  
 165 <223> OTHER INFORMATION: probe  
 W--> 166 <400> SEQUENCE: 5  
 167 ctggcactgg gcatgtcaca caac  
 E--> 173 bhc 04 1 090 sp/ngb/nt/v2006-09-15  
 E--> 175 - 1 -

Does Not Comply  
Corrected Diskette Needed

24

VARIABLE LOCATION SUMMARY

DATE: 10/06/2006

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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; N Pos. 2966,2967,2968,2969,2970,2971,2972

Seq#:5; N Pos. 29,32

## VERIFICATION SUMMARY

DATE: 10/06/2006

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Input Set : A:\004974.01218 sequence listing.txt

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L:8 M:283 W: Missing Blank Line separator, <130> field identifier  
L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:18 M:283 W: Missing Blank Line separator, <210> field identifier  
L:22 M:283 W: Missing Blank Line separator, <220> field identifier  
L:26 M:283 W: Missing Blank Line separator, <400> field identifier  
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2940  
L:87 M:283 W: Missing Blank Line separator, <400> field identifier  
L:148 M:283 W: Missing Blank Line separator, <220> field identifier  
L:150 M:283 W: Missing Blank Line separator, <400> field identifier  
L:156 M:283 W: Missing Blank Line separator, <220> field identifier  
L:158 M:283 W: Missing Blank Line separator, <400> field identifier  
L:164 M:283 W: Missing Blank Line separator, <220> field identifier  
L:166 M:283 W: Missing Blank Line separator, <400> field identifier  
L:173 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5  
L:173 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5  
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:24  
L:173 M:254 E: No. of Bases conflict, LENGTH:Input:-15 Counted:40 SEQ:5  
L:173 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10  
L:173 M:112 C: (48) String data converted to lower case,  
M:254 Repeated in SeqNo=5  
L:175 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:40 SEQ:5